IN THE SPECIFICATION:

On page 1, please delete the current title of the application and replace it with the following new title:

CYSTEINE VARIANTS OF GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR

On page 1, immediately following the title, please insert the following new subheading and paragraph:

Cross-Reference to Related Applications

This application is a continuation of U.S. Application Serial No. 10/400,377, filed March 26, 2003, which is a divisional of U.S. Application Serial No. 09/462,941, filed January 14, 2000, now U.S. Patent No. 6,608,183, which is a national stage application under 35 U.S.C. § 371 of PCT Application Serial No. PCT/US98/14497, filed July 13, 1998, which claims the benefit of priority from U.S. Provisional Application Serial No. 60/052,516, filed July 14, 1997. Each of the above-identified applications and patent is incorporated herein by reference in its entirety.

On page 1, following the paragraph added above entitled "Cross-Reference to Related Applications", please insert the following subheading and paragraph:

Government Support

This invention was made in part with government support under Grant Nos. 1R43 CA84850 and 2R44 CA84850, each awarded by the National Institutes of Health. The government has certain rights in the invention.

On page 47, line 12, please insert the following new paragraph:

Walter et al., 1992, *J. Mol. Biol.* 224:1075-1085 (see Fig. 4 of this publication) provides an alignment of amino acid sequences of granulocyte-macrophage colony-stimulating factor from different species and the position of the four alpha helices relative to these sequences. As can be

seen in Fig. 4 of Walter et al., the positions of the four helical regions and the intervening (loop) regions, as well as the regions preceding Helix A and following Helix D, are located within the sequence for human granulocyte-macrophage colony-stimulating factor at the following positions (positions given relative to SEQ ID NO:8):

Preceding Helix A = residues 1-12;

Helix A = residues 13-27;

A-B loop = residues 28-54;

Helix B = residues 55-65;

B-C loop = residues 66-73;

Helix C = residues 74-86;

C-D loop = residues 87-102;

Helix D = residues 103-116;

Following Helix D = residues 117-127.